

General information

Entry name **HYAL4_HUMAN**
 Accession number **[Q2M3T9](#), [Q9UL99](#), [Q9Y6T9](#)**
 Integrated 11-SEP-2007, UniProtKB/Swiss-Prot.
 Sequence update 11-SEP-2007, sequence version 2
 Annotation update 11-SEP-2007, entry version 16
 UniSave **[Q2M3T9](#), [Q9UL99](#), [Q9Y6T9](#)**
 UniRef100 **[UniRef100_Q2M3T9](#)**
 UniParc **[UPI000006F62B](#)**

Description and origin of the Protein

Description Hyaluronidase-4 (EC [3.2.1.35](#)) (Hyal-4) (Hyaluronoglucosaminidase-4).
 Gene name(s) **HYAL4**
 Organism source **Homo sapiens (Human)**.
 Taxonomy Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutl
 Haplorrhini; Catarrhini; Hominidae; Homo.
 NCBI TaxID **[9606](#)**

References

- [1] Csoka,A.B., Scherer,S.W., Stern,R.,
**Expression analysis of six paralogous human hyaluronidase
 chromosomes 3p21 and 7q31.**
 (1999) *Genomics* **60**:356-361
 Position NUCLEOTIDE SEQUENCE [MRNA], AND TISSUE SPECIFICITY.
 DOI [10.1006/geno.1999.5876](#);
- [2] Hillier,L.W., Fulton,R.S., Fulton,L.A., Graves,T.A., Pepin,K.H., Wagner-McPherson
 Walker,R., Wylie,K., Sekhon,M., Becker,M.C., O'Laughlin,M.D., Schaller,M.E., Fe
 Nash,W.E., Cordes,M., Du,H., Sun,H., Edwards,J., Bradshaw-Cordum,H., Ali,J., An
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 Kent,W.J., Furey,T.S., Baertsch,R.A., Brent,M.R., Keibler,E., Flicek,P., Bork,P., Su
 Torrents,D., Chinwalla,A.T., Gish,W.R., Eddy,S.R., McPherson,J.D., Olson,M.V., E
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The DNA sequence of human chromosome 7.
 (2003) *Nature* **424**:157-164
 Position NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

DOI [10.1038/nature01782](https://doi.org/10.1038/nature01782);

- [3] Scherer, S.W., Cheung, J., MacDonald, J.R., Osborne, L.R., Nakabayashi, K., Herbrick, Skaug, J., Khaja, R., Zhang, J., Hudek, A.K., Li, M., Haddad, M., Duggan, G.E., Fernand Christopoulos, C.C., Choufani, S., Kwasnicka, D., Zheng, X.H., Lai, Z., Nusskern, D., Z Nowaczyk, M.J., Teshima, I., Chitayat, D., Shuman, C., Weksberg, R., Zackai, E.H., Gr Rahman, N., Friedman, J.M., Heng, H.H.Q., Pelicci, P.G., Lo-Coco, F., Belloni, E., Sha Gusella, J.F., Bruns, G.A.P., Korf, B.R., Quade, B.J., Ligon, A.H., Ferguson, H., Higgin Lemyre, E., Farra, C.G., Kim, H.-G., Summers, A.M., Gripp, K.W., Roberts, W., Szatm Teebi, A., Minassian, B.A., Kere, J., Armengol, L., Pujana, M.A., Estivill, X., Wilson, M Boright, A.P., Zlotorynski, E., Kerem, B., Kroisel, P.M., Petek, E., Oscier, D.G., Mould, Rommens, J.M., Vincent, J.B., Venter, J.C., Li, P.W., Mural, R.J., Adams, M.D., Tsui, L
Human chromosome 7: DNA sequence and biology.
(2003) *Science* **300**:767-772

Position NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

DOI [10.1126/science.1083423](https://doi.org/10.1126/science.1083423);

- [4]
The status, quality, and expansion of the NIH full-length cDI Gene Collection (MGC).
(2004) *Genome Res.* **14**:2121-2127

Position NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA], AND VARIATION
Comments TISSUE=Cerebellum;

DOI [10.1101/gr.2596504](https://doi.org/10.1101/gr.2596504);

- [5] Jedrzejewski, M.J., Stern, R.,
Structures of vertebrate hyaluronidases and their unique endohydrolysis.
(2005) *Proteins* **61**:227-238

Position FUNCTION, AND 3D-STRUCTURE MODELING.

DOI [10.1002/prot.20592](https://doi.org/10.1002/prot.20592);

Comments

FUNCTION	Endo-hyaluronidase that degrades hyaluronan to smaller oligosaccharide
CATALYTIC ACTIVITY	Random hydrolysis of 1->4-linkages between N- acetyl-beta-D-glucosamine and hyaluronate.
SUBCELLULAR LOCATION	Membrane; Multi-pass membrane protein (Potential).
TISSUE SPECIFICITY	Detected in placenta and skeletal muscle.
SIMILARITY	Belongs to the glycosyl hydrolase 56 family.

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Database cross-references

[AF009010](#); [AAC98883.1](#); -; mRNA.

	AC006029 ; AAD43186.1 ; -, Genomic_DNA.
	CH236947 ; EAL24331.1 ; -, Genomic_DNA.
EMBL	BC104788 ; AAI04789.1 ; -, mRNA.
	BC104790 ; AAI04791.1 ; -, mRNA.
UniGene	Hs.28673 ; -.
Ensembl	ENSG00000106302 ; Homo sapiens.
HGNC	HGNC: 5323 ; HYAL4.
MIM	604510 ; gene.
PharmGKB	PA29574 ; -.
ArrayExpress	Q2M3T9 ; -.
	IPR013785 ; Aldolase_TIM.
	IPR002355 ; Cu_oxidase_Cu_BS.
InterPro	IPR006210 ; EGF.
	IPR013032 ; EGF_like_reg.
	IPR001968 ; Glyco_hydro_56.
	IPR001439 ; Glyco_hydro_56_PH20.
Gene3D	G3DSA:3.20.20.70 ; Aldolase_TIM; 1.
PANTHER	PTHR11769 ; Glyco_hydro_56; 1.
Pfam	PF01630 ; Glyco_hydro_56; 1.
	PR00846 ; GLHYDRLASE56.
PRINTS	PR00848 ; SPERMPH20.
ProDom	PD003549 ; Glyco_hydro_56; 1.
SMART	SM00181 ; EGF; 1.
PROSITE	PS00022 ; EGF_1; 1.
	PS01186 ; EGF_2; 1.

Protein Existence

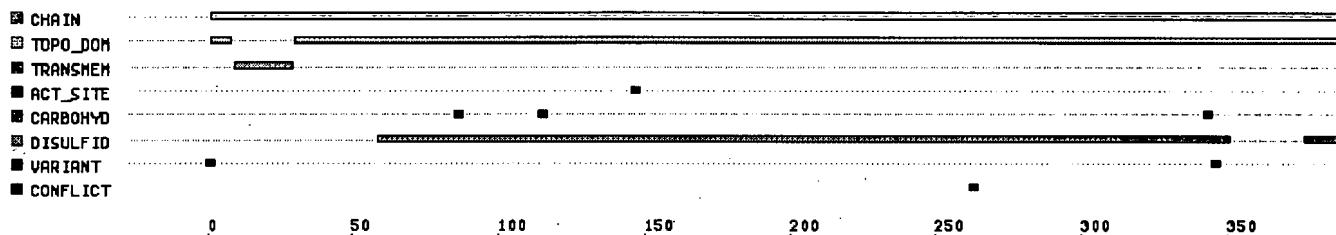
2: Evidence at transcript level;

Keywords

[EGF-like domain](#); [Glycoprotein](#); [Glycosidase](#); [Hydrolase](#); [Membrane](#); [Polymorphism](#); [Transmembrane](#);

Features

[Features compressed](#) | [Features expanded](#)



Key	Begin	End	Length	Description
<u>CHAIN</u>	1	481	481	Hyaluronidase-4. /FTId= <u>PRO_0000301999</u> .
<u>TOPO_DOM</u>	1	8	8	Cytoplasmic (Potential).
<u>TRANSMEM</u>	9	29	21	Potential.
<u>TOPO_DOM</u>	30	453	424	Extracellular (Potential).
<u>TRANSMEM</u>	454	474	21	Potential.
<u>TOPO_DOM</u>	475	481	7	Cytoplasmic (Potential).
<u>ACT_SITE</u>	147	147	1	Proton donor (By similarity).
<u>CARBOHYD</u>	86	86	1	N-linked (GlcNAc...) (Potential).
<u>CARBOHYD</u>	115	115	1	N-linked (GlcNAc...) (Potential).
<u>CARBOHYD</u>	343	343	1	N-linked (GlcNAc...) (Potential).
<u>DISULFID</u>	59	351	293	By similarity.
<u>DISULFID</u>	223	237	15	By similarity.
<u>DISULFID</u>	376	387	12	By similarity.
<u>DISULFID</u>	381	435	55	By similarity.
<u>DISULFID</u>	437	446	10	By similarity.
<u>VARIANT</u>	1	1	1	M -> V (in dbSNP:rs12672205). /FTId= <u>VAR_034935</u>
<u>VARIANT</u>	346	346	1	A -> S (in dbSNP:rs6949082). /FTId= <u>VAR_034936</u> .
<u>CONFLICT</u>	263	263	1	G -> C (in Ref. 1; AAC98883).

Sequence information

Length: **481 aa**, molecular weight: **54249 Da**, CRC64 checksum: **9D530009AA89**

Display Format ☒ FASTA ☐ GCG ☐ PIR ☐ Swiss-Prot ☐ Pretty

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>uniprot|Q2M3T9|HYAL4_HUMAN Hyaluronidase-4 (EC 3.2.1.35) (Hyal-4) (Hyaluronoglu
MKVLSEGLKLCVVQPVHLTSWLLIFFILKSISCLKPARLPPIYQRKPFIAAWNAPTDQCL
IKYNLRLNLKMFVIGSPLAKARGQNVTFYVNRNLGYYPWYTSQGVPIINGGLPQNISLQV
HLEKADQDINYYIPAEDFSGLAVIDWEYWRPQWARNWNSKDVYRQKSRKLISDMGKNVSA
TDIEYLAKVTFEESAKAFMKETIKLGIKSRPKGLWGYYLYPDCHNYNVYAPNYSGSCPED
EVLRRNELSWLWNSSAALYPSIGVWVSLGDSENILRFSKFRVHESMRISTMTSHDYALPV
FVYTRLGYRDEPLFFLSKQDLVSTIGESAALGAAGIVIWGMNLTASKANCTKVQFVSS
DLGSYIANVTTRAAEVCSLHLCRNNGRCIRKMWNAPSILHLPASYHIEASEDFTEVKGK
ASDSDLAVMADTFSCHCYQGYEGADCREIKTADGCSGVSPSPGSLMTLCLLLLASYSIQ
L
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